



SEQUENCE LISTING

<110> Walke, D. Wade  
Friddle, Carl Johan  
Mathur, Brian  
Turner, C. Alexander Jr.

<120> Novel Human GABA Receptors and  
Polynucleotides Encoding the Same

<130> LEX-0195-USA

<150> US 60/214,083  
<151> 2000-06-27

<160> 5

<170> FastSEQ for Windows Version 4.0

*Sub B*  
<210> 1  
<211> 1398  
<212> DNA  
<213> homo sapiens

<400> 1

atgggtcctt	tgaaaagcttt	tctcttctcc	ccttttcttc	tgcgaggatca	aagttagaggg	60
gtgagggttgg	tcttcttgg	actgacccctg	catttggaa	actgtgttga	taaggcagat	120
gatgaagatg	atgaggattt	aacggtaac	aaaacctggg	tcttggccccc	aaaaattcat	180
gaaggagata	tcacacaaaat	tctgaattca	ttgcttcaag	gctatgacaa	taaacttcgt	240
ccagatata	gagtggggcc	cacrgtaatt	gaaactgatg	tttatgtaaa	cagcattgg	300
ccagttgatc	caattaat	ggaatataca	atagatataa	tttttgc	aacctgg	360
gacagtgcgtt	taaaattcaa	tagtaccat	aaagtgc	tgcttaacag	taatatgg	420
ggaaaaattt	ggattcctga	cacttcttc	agaaactcaa	gaaaatctga	tgctcactgg	480
ataacaactc	ctaatcg	gttcgaatt	tggaatgatg	gacgaggatct	gtatactcta	540
agattgacaa	ttaatgcaga	atgttatctt	tagcttcata	actttccat	ggatgaacat	600
tcctgtccac	tggaattttc	aagctatgga	taccctaaaa	atgaaattga	gtataagtgg	660
aaaaagccct	ccgtagaagt	ggctgatc	aaatactgga	gattatata	gtttgcattt	720
gtagggttac	ggaactcaac	tgaaatca	cacacgatct	cgwgggatta	kgttatcatg	780
acaattttt	ttgacctgag	cagaagaatg	ggtatattca	ctattcagac	ctacattcca	840
tgcattctga	cagttgttct	ttcttgggt	tcttttgg	tcaataaaga	tgca	900
gcaagaacat	cgttgggtat	cactacagt	ctgactatga	caaccctgag	tacaattg	960
aggaagtctt	tacctaaggt	ttcttatgt	actgcgatgg	atctctt	ttctgtt	1020
ttcattttt	ttttgc	cttgatggaa	tatggAACCT	tgcattattt	taccagcaac	1080
caaaaaggaa	agactgctac	taaagacaga	aagctaaaa	ataaaagc	ctc gatgactc	1140
ggtctccatc	ctggatccac	tctgattcca	atgaaataata	tttctgt	gcaagaagat	1200
gattatgggt	atcgtgtt	ggagggcaaa	gattgt	gcca	ttgctt	1260
gactgcagaa	caggatctg	gagggagga	aggata	acata	tacgcattgc	1320
tcttattct	aatattttt	cccaaccgct	tttgc	ttgtt	caaaattgac	1380
ggctatctt	acttataa					1398

<210> 2  
<211> 465  
<212> PRT  
<213> homo sapiens

<400> 2

Met Gly Pro Leu Lys Ala Phe Leu Phe Ser Pro Phe Leu Leu Arg Ser  
1 5 10 15  
Gln Ser Arg Gly Val Arg Leu Val Phe Leu Leu Leu Thr Leu His Leu  
20 25 30  
Gly Asn Cys Val Asp Lys Ala Asp Asp Glu Asp Asp Glu Asp Leu Thr  
35 40 45  
Val Asn Lys Thr Trp Val Leu Ala Pro Lys Ile His Glu Gly Asp Ile  
50 55 60  
Thr Gln Ile Leu Asn Ser Leu Leu Gln Gly Tyr Asp Asn Lys Leu Arg  
65 70 75 80  
Pro Asp Ile Gly Val Arg Pro Thr Val Ile Glu Thr Asp Val Tyr Val  
85 90 95  
Asn Ser Ile Gly Pro Val Asp Pro Ile Asn Met Glu Tyr Thr Ile Asp  
100 105 110  
Ile Ile Phe Ala Gln Thr Trp Phe Asp Ser Arg Leu Lys Phe Asn Ser  
115 120 125  
Thr Met Lys Val Leu Met Leu Asn Ser Asn Met Val Gly Lys Ile Trp  
130 135 140  
Ile Pro Asp Thr Phe Phe Arg Asn Ser Arg Lys Ser Asp Ala His Trp  
145 150 155 160  
Ile Thr Thr Pro Asn Arg Leu Leu Arg Ile Trp Asn Asp Gly Arg Val  
165 170 175  
Leu Tyr Thr Leu Arg Leu Thr Ile Asn Ala Glu Cys Tyr Leu Gln Leu  
180 185 190  
His Asn Phe Pro Met Asp Glu His Ser Cys Pro Leu Glu Phe Ser Ser  
195 200 205  
Tyr Gly Tyr Pro Lys Asn Glu Ile Glu Tyr Lys Trp Lys Lys Pro Ser  
210 215 220  
Val Glu Val Ala Asp Pro Lys Tyr Trp Arg Leu Tyr Gln Phe Ala Phe  
225 230 235 240  
Val Gly Leu Arg Asn Ser Thr Glu Ile Thr His Thr Ile Ser Gly Asp  
245 250 255  
Tyr Val Ile Met Thr Ile Phe Phe Asp Leu Ser Arg Arg Met Gly Tyr  
260 265 270  
Phe Thr Ile Gln Thr Tyr Ile Pro Cys Ile Leu Thr Val Val Leu Ser  
275 280 285  
Trp Val Ser Phe Trp Ile Asn Lys Asp Ala Val Pro Ala Arg Thr Ser  
290 295 300  
Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Leu Ser Thr Ile Ala  
305 310 315 320  
Arg Lys Ser Leu Pro Lys Val Ser Tyr Val Thr Ala Met Asp Leu Phe  
325 330 335  
Val Ser Val Cys Phe Ile Phe Val Phe Ala Ala Leu Met Glu Tyr Gly  
340 345 350  
Thr Leu His Tyr Phe Thr Ser Asn Gln Lys Gly Lys Thr Ala Thr Lys  
355 360 365  
Asp Arg Lys Leu Lys Asn Lys Ala Ser Met Thr Pro Gly Leu His Pro  
370 375 380  
Gly Ser Thr Leu Ile Pro Met Asn Asn Ile Ser Val Pro Gln Glu Asp  
385 390 395 400  
Asp Tyr Gly Tyr Gln Cys Leu Glu Gly Lys Asp Cys Ala Ser Phe Phe  
405 410 415  
Cys Cys Phe Glu Asp Cys Arg Thr Gly Ser Trp Arg Glu Gly Arg Ile  
420 425 430  
His Ile Arg Ile Ala Lys Ile Asp Ser Tyr Ser Arg Ile Phe Phe Pro

435 440 445  
Thr Ala Phe Ala Leu Phe Asn Leu Val Tyr Trp Val Gly Tyr Leu Tyr  
450 455 460

Leu  
465

<210> 3  
<211> 771  
<212> DNA  
<213> homo sapiens

<400> 3  
atgggtcctt tgaaagcttt tctttctcc cctttcttc tgccggagtca aagtagaggg 60  
gtgagggtgg tttttttgtt actgaccctg catttggaa actgtgttga taaggcagat 120  
gatgaagatg atgaggattt aacggtaac aaaacctggg tcttggccccc aaaaattcat 180  
gaaggagata tcacacacaat tctgaattca ttgcttcaag gctatgacaa taaacttcgt 240  
ccagatatacg gagtgaggcc cacagtaatt gaaactgtatg tttatgtaaa cagcattgga 300  
ccagttgatc caattatataat ggaatataca atagatataa tttttgccc aacctggttt 360  
gacagtgcgtt taaaattcaa tagtaccatg aaagtgccta tgcttaacag taatatggtt 420  
ggaaaaattt ggattcttga cacttcttc agaaactcaa gaaaatctga tgctcactgg 480  
ataacaactc ctaatcgatc gtttgcattt tggatgtatg gacgagttct gtatactcta 540  
agattgacaa ttaatgcaga atgttatctt cagcttcata actttccat ggtgaacat 600  
tcctgtccac tggatatttc aagctatgga taccctaaaa atgaaatttga gtataagtgg 660  
aaaaagccct ccgtagaagt ggctgatcct aaatactgga gattatatca gtttgcattt 720  
gtagggttac ggaactcaad tgaaatcact cacacgatct ctggggattt g 771

<210> 4  
<211> 256  
<212> PRT  
<213> homo sapiens

<400> 4  
Met Gly Pro Leu Lys Ala Phe Leu Phe Ser Pro Phe Leu Leu Arg Ser  
1 5 10 15  
Gln Ser Arg Gly Val Arg Leu Val Phe Leu Leu Leu Thr Leu His Leu  
20 25 30  
Gly Asn Cys Val Asp Lys Ala Asp Asp Glu Asp Asp Glu Asp Leu Thr  
35 40 45  
Val Asn Lys Thr Trp Val Leu Ala Pro Lys Ile His Glu Gly Asp Ile  
50 55 60  
Thr Gln Ile Leu Asn Ser Leu Leu Gln Gly Tyr Asp Asn Lys Leu Arg  
65 70 75 80  
Pro Asp Ile Gly Val Arg Pro Thr Val Ile Glu Thr Asp Val Tyr Val  
85 90 95  
Asn Ser Ile Gly Pro Val Asp Pro Ile Asn Met Glu Tyr Thr Ile Asp  
100 105 110  
Ile Ile Phe Ala Gln Thr Trp Phe Asp Ser Arg Leu Lys Phe Asn Ser  
115 120 125  
Thr Met Lys Val Leu Met Leu Asn Ser Asn Met Val Gly Lys Ile Trp  
130 135 140  
Ile Pro Asp Thr Phe Phe Arg Asn Ser Arg Lys Ser Asp Ala His Trp  
145 150 155 160  
Ile Thr Thr Pro Asn Arg Leu Leu Arg Ile Trp Asn Asp Gly Arg Val  
165 170 175  
Leu Tyr Thr Leu Arg Leu Thr Ile Asn Ala Glu Cys Tyr Leu Gln Leu  
180 185 190

His Asn Phe Pro Met Asp Glu His Ser Cys Pro Leu Glu Phe Ser Ser  
 195 200 205  
 Tyr Gly Tyr Pro Lys Asn Glu Ile Glu Tyr Lys Trp Lys Lys Pro Ser  
 210 215 220  
 Val Glu Val Ala Asp Pro Lys Tyr Trp Arg Leu Tyr Gln Phe Ala Phe  
 225 230 235 240  
 Val Gly Leu Arg Asn Ser Thr Glu Ile Thr His Thr Ile Ser Gly Asp  
 245 250 255

<210> 5

<211> 1568

<212> DNA

<213> homo sapiens

<400> 5

ggtgcactgc cttccacac tctcccttct gtactcagcc agctgctgct gaggtggag 60  
 gaaaagtccct ggctgggaga atttagctag tgcagcacac gtaaaaaagc gattccgatg 120  
 ggtcctttga aagctttct cttctccct tttcttctgc ggagtcaaag tagaggggtg 180  
 aggttggctct tcttggtaact gaccctgcatttggaaact gtgttgataa ggcagatgat 240  
 gaagatgatg aggatthaac ggtgaacaaa acctgggtct tggcccaaaa aattcatgaa 300  
 ggagatatac cacaatttctt gaattcatttgc cttcaaggct atgacaataa acttcgtcca 360  
 gatataaggag tgaggccac rgttaatttgc actgtatgtt atgtaaacag cattggacca 420  
 gttgatccaa ttaatatggaa atatacaata gatataattt ttgccccaaac ctggtttgac 480  
 agtcgtttaa aattcaatag taccatggaa gtgcttatgc ttaacagtaa tatggttggaa 540  
 aaaatttggaa ttccctgacac tttcttcaga aactcaagaa aatctgatgc tcactggata 600  
 acaactccta atcgtctgct tcgaatttgg aatgatggac gagttctgta tactctaaga 660  
 ttgacaatttta atgcagaatgtt ttagtcttgc cttcataact ttccccatggaa tgaacattcc 720  
 tggccactgg aattttcaag ctatggatc cctaaaaatg aaattgagta taagtggaaa 780  
 aagccctccg tagaagtggc tgatcctaaa tactggagat tatatcgat tgcattttgt 840  
 gggttacgga actcaactga aatcactcac acgatctcg gggattakgt tatcatgaca 900  
 atttttttttgc acctgagcag aagaatggaa tatttcacta ttccagaccta cattccatgc 960  
 attctgacac ttgttcttgc ttgggtgtct tttggatca ataaagatgc agtcgtcgca 1020  
 agaacatcgat tgggtatcac tacagttctg actatgacaa ccctgagttac aatttgcagg 1080  
 aagtctttac ctaaggttgc ttatgtgact tgcgtggatc tctttgttgc ttgttggatc 1140  
 atttttttttgc ttgcagccctt gatggaatat ggaaccttgc attattttac cagcaaccaa 1200  
 aaaggaaaaga ctgctactaa agacagaaaag ctaaaaaata aagcctcgat gactcctgg 1260  
 ctccatcctg gatccactct gattccaatg aataatattt ctgtgccgca agaagatgat 1320  
 tatgggtatc agtggggatc gggcaaaatg tgcgtggatc tctttgttgc ttgttggatc 1380  
 tgcagaacac gatcttggag ggaaggaaagg atacacatac gcattgcca aatttgcact 1440  
 tattcttagaa tattttttcc aaccgctttt gcccgttca acttgggttta ttgggttggc 1500  
 tatctttact tataaaatctt acttcataag caaaaatcaa aagaagtctt gacttaaattt 1560  
 tcaagtag 1568